IN THE CLAIMS:

Please amend the following claims as follows:

A1

1. (Amended) A method for analyzing an intestinal bacterial flora of a subject, comprising:

a nucleic acid amplifying step of amplifying nucleic acid of an intestinal bacterial group in a sample extracted from the subject with a specific PCR primer; and

an analyzing step of analyzing the intestinal bacterial flora on the basis of an amplified fragment obtained in said nucleic acid amplifying step, wherein

said specific primer is a primer having a specific amplification probability.

A2

5. (amended) A method for analyzing an intestinal bacterial flora of a subject, comprising:

a nucleic acid amplifying step of amplifying nucleic acid of an intestinal bacterial group in a sample extracted from the subject with a specific PCR primer; and

an analyzing step of analyzing the intestinal bacterial flora on the basis of an amplified fragment obtained in said nucleic acid amplifying step, wherein

hybridization with said amplified fragment is performed using a plurality of probes so that analysis of the intestinal bacterial flora is performed based upon presence/absence of formation thereof in said analyzing step, and

said probes are arranged on specific positions in a detector.

6. (amended) The method for analyzing an intestinal bacterial flora according to claim 4 or 5, wherein nucleic acid amplified from each intestinal bacterium with the PCR primer employed in said nucleic acid amplifying step is used as a probe.

7. (amended) The method for analyzing an intestinal bacterial flora according to claim 4 or 5, wherein the nucleic acid obtained in said nucleic acid amplifying step is denatured before introduction into said detector.

A2 cont.

8. (amended) The method for analyzing an intestinal bacterial flora according to claim 4 or 5, wherein a set temperature of said detector is arbitrarily changeable according to an instruction from a temperature controller.

9. (amended) The method for analyzing an intestinal bacterial flora according to claim 5, wherein said specific PCR primer has a sequence capable of amplifying a nucleic acid region coding 16SrRNA of said intestinal bacterium.